

SEQUENCE LISTING

<110> Auckland UniServices Limited

<120> Superantigens

<130> 25426 MRB

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<150> NZ 333589

<151> 1998-12-24

<160> 8

<170> PatentIn Ver. 2.1

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<211> 702

<212> DNA

<213> Streptococcus pyogenes

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<221> CDS

<222> (1)..(699)

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1				5					10					15		

ata	att	tct	cgt	cct	gtg	ttt	gga	tta	gaa	gta	gat	aat	aat	tcc	gtt	96
Ile	Ile	Ser	Arg	Pro	Val	Phe	Gly	Leu	Glu	Val	Asp	Asn	Asn	Ser	Leu	
			20					25						30		

cta	agg	aat	atc	tat	agt	acg	att	gta	tat	gaa	tat	tca	gat	ata	gta	144
Leu	Arg	Asn	Ile	Tyr	Ser	Thr	Ile	Val	Tyr	Glu	Tyr	Ser	Asp	Ile	Val	
		35						40						45		

att	gat	ttt	aaa	acc	agt	cat	aac	tta	gtg	act	aag	aaa	ctt	gat	gtt	192
Ile	Asp	Phe	Lys	Thr	Ser	His	Asn	Leu	Val	Thr	Lys	Lys	Leu	Asp	Val	
		50					55					60				

aga	gat	gct	aga	gat	ttc	ttt	att	aac	tcc	gaa	atg	gac	gaa	tat	gca	240
Arg	Asp	Ala	Arg	Asp	Phe	Phe	Ile	Asn	Ser	Glu	Met	Asp	Glu	Tyr	Ala	
65						70					75				80	

1 5 10 15
 Ile Ile Ser Arg Pro Val Phe Gly Leu Glu Val Asp Asn Asn Ser Leu
 20 25 30
 Leu Arg Asn Ile Tyr Ser Thr Ile Val Tyr Glu Tyr Ser Asp Ile Val
 35 40 45
 Ile Asp Phe Lys Thr Ser His Asn Leu Val Thr Lys Lys Leu Asp Val
 50 55 60
 Arg Asp Ala Arg Asp Phe Phe Ile Asn Ser Glu Met Asp Glu Tyr Ala
 65 70 75 80
 Ala Asn Asp Phe Lys Thr Gly Asp Lys Ile Ala Val Phe Ser Val Pro
 85 90 95
 Phe Asp Trp Asn Tyr Leu Ser Lys Gly Lys Val Thr Ala Tyr Thr Tyr
 100 105 110
 Gly Gly Ile Thr Pro Tyr Gln Lys Thr Ser Ile Pro Lys Asn Ile Pro
 115 120 125
 Val Asn Leu Trp Ile Asn Gly Lys Gln Ile Ser Val Pro Tyr Asn Glu
 130 135 140
 Ile Ser Thr Asn Lys Thr Thr Val Thr Ala Gln Glu Ile Asp Leu Lys
 145 150 155 160
 Val Arg Lys Phe Leu Ile Ala Gln His Gln Leu Tyr Ser Ser Gly Ser
 165 170 175
 Ser Tyr Lys Ser Gly Arg Leu Val Phe His Thr Asn Asp Asn Ser Asp
 180 185 190
 Lys Tyr Ser Phe Asp Leu Phe Tyr Val Gly Tyr Arg Asp Lys Glu Ser
 195 200 205
 Ile Phe Lys Val Tyr Lys Asp Asn Lys Ser Phe Asn Ile Asp Lys Ile
 210 215 220
 Gly His Leu Asp Ile Glu Ile Asp Ser
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<213> Streptococcus pyogenes

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tat gga agt caa tta gct tat gca gat gaa aat tta aaa gat tta aaa	96
Tyr Gly Ser Gln Leu Ala Tyr Ala Asp Glu Asn Leu Lys Asp Leu Lys	
20 25 30	
aga agt tta aga ttt gcc tat aat att acc cca tgc gat tat gaa aat	144
Arg Ser Leu Arg Phe Ala Tyr Asn Ile Thr Pro Cys Asp Tyr Glu Asn	
35 40 45	
gta gaa att gca ttt gtt act aca aat agc ata cat att aat act aaa	192
Val Glu Ile Ala Phe Val Thr Thr Asn Ser Ile His Ile Asn Thr Lys	
50 55 60	
caa aaa aga tcg gaa tgt att ctt tat gtt gat tct att gta tct tta	240
Gln Lys Arg Ser Glu Cys Ile Leu Tyr Val Asp Ser Ile Val Ser Leu	
65 70 75 80	
ggc att act gat cag ttt ata aaa ggg gat aag gtc gat gtt ttt ggt	288
Gly Ile Thr Asp Gln Phe Ile Lys Gly Asp Lys Val Asp Val Phe Gly	
85 90 95	
ctc cct tat aat ttt tcc cca cct tat gta gat aat att tat ggt ggt	336
Leu Pro Tyr Asn Phe Ser Pro Pro Tyr Val Asp Asn Ile Tyr Gly Gly	
100 105 110	
att gta aaa cat tcg aat caa gga aat aaa tca tta cag ttt gta gga	384
Ile Val Lys His Ser Asn Gln Gly Asn Lys Ser Leu Gln Phe Val Gly	
115 120 125	
att tta aat caa gat ggg aaa gaa act tat ttg ccc tct gag gct gtt	432
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130 135 140	
cgc ata aaa aag aaa cag ttt act tta cag gaa ttt gat ttt aaa ata	480
Arg Ile Lys Lys Lys Gln Phe Thr Leu Gln Glu Phe Asp Phe Lys Ile	
145 150 155 160	

Ile Val Lys His Ser Asn Gln Gly Asn Lys Ser Leu Gln Phe Val Gly
 115 120 125

Ile Leu Asn Gln Asp Gly Lys Glu Thr Tyr Leu Pro Ser Glu Ala Val
 130 135 140

Arg Ile Lys Lys Lys Gln Phe Thr Leu Gln Glu Phe Asp Phe Lys Ile
 145 150 155 160

Arg Lys Phe Leu Met Glu Lys Tyr Asn Ile Tyr Asp Ser Glu Ser Arg
 165 170 175

Tyr Thr Ser Gly Ser Leu Phe Leu Ala Thr Lys Asp Ser Lys His Tyr
 180 185 190

Glu Val Asp Leu Phe Asn Lys Asp Asp Lys Leu Leu Ser Arg Asp Ser
 195 200 205

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<222> (1)..(708)

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 Met Ile Ile Cys Leu Ser Phe Leu Leu Tyr Ser Asn Val Val Gln Ala
 20 25 30

aat tct tat aat aca acc aat aga cat aat cta gaa tcg ctt tat aag 144
 Asn Ser Tyr Asn Thr Thr Asn Arg His Asn Leu Glu Ser Leu Tyr Lys
 35 40 45

cat gat tct aac ttg att gaa gcc gat agt ata aaa aat tct cca gat 192
His Asp Ser Asn Leu Ile Glu Ala Asp Ser Ile Lys Asn Ser Pro Asp
50 55 60

att gta aca agc cat atg ttg aaa tat agt gtc aag gat aaa aat ttg 240
Ile Val Thr Ser His Met Leu Lys Tyr Ser Val Lys Asp Lys Asn Leu
65 70 75 80

tca gtt ttt ttt gag aaa gat tgg ata tca cag gaa ttc aaa gat aaa 288
Ser Val Phe Phe Glu Lys Asp Trp Ile Ser Gln Glu Phe Lys Asp Lys
85 90 95

gaa gta gat att tat gct cta tct gca caa gag gtt tgt gaa tgt cca 336
Glu Val Asp Ile Tyr Ala Leu Ser Ala Gln Glu Val Cys Glu Cys Pro
100 105 110

ggg aaa agg tat gaa gcg ttt ggt gga att aca tta act aat tca gaa 384
Gly Lys Arg Tyr Glu Ala Phe Gly Gly Ile Thr Leu Thr Asn Ser Glu
115 120 125

aaa aaa gaa att aaa gtt cct gta aac gtg tgg gat aaa agt aaa caa 432
Lys Lys Glu Ile Lys Val Pro Val Asn Val Trp Asp Lys Ser Lys Gln
130 135 140

cag ccg cct atg ttt att aca gtc aat aaa ccg aaa gta acc gct cag 480
Gln Pro Pro Met Phe Ile Thr Val Asn Lys Pro Lys Val Thr Ala Gln
145 150 155 160

gaa gtg gat ata aaa gtt aga aag tta ttg att aag aaa tac gat atc 528
Glu Val Asp Ile Lys Val Arg Lys Leu Leu Ile Lys Lys Tyr Asp Ile
165 170 175

tat aat aac cgg gaa caa aaa tac tct aaa gga act gtt acc tta gat 576
Tyr Asn Asn Arg Glu Gln Lys Tyr Ser Lys Gly Thr Val Thr Leu Asp
180 185 190

tta aat tca ggt aaa gat att gtt ttt gat ttg tat tat ttt ggc aat 624
Leu Asn Ser Gly Lys Asp Ile Val Phe Asp Leu Tyr Tyr Phe Gly Asn
195 200 205

gga gac ttt aat agc atg cta aaa ata tat tcc aat aac gag aga ata 672
Gly Asp Phe Asn Ser Met Leu Lys Ile Tyr Ser Asn Asn Glu Arg Ile
210 215 220

gac tca act caa ttt cat gta gat gtg tca atc agc taa 711
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             20             25             30

aat tta cta ata gat gga gtc cag caa aaa aca cta ata aat ccc ata 144
Asn Leu Leu Ile Asp Gly Val Gln Gln Lys Thr Leu Ile Asn Pro Ile
      35             40             45

aaa ata gat aaa cct att ttt acg att caa gaa ttt gac ttc aaa atc 192
Lys Ile Asp Lys Pro Ile Phe Thr Ile Gln Glu Phe Asp Phe Lys Ile
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aga caa tat ctt atg caa aca tac aaa att tat gat cct aat tct cca 240
Arg Gln Tyr Leu Met Gln Thr Tyr Lys Ile Tyr Asp Pro Asn Ser Pro
      65             70             75             80

tac ata aaa ggg caa tta gaa att gcg atc aat ggc aat aaa cat gaa 288
Tyr Ile Lys Gly Gln Leu Glu Ile Ala Ile Asn Gly Asn Lys His Glu
             85             90             95

agt ttt aac tta tat gat gca acc tca tct agt aca agg agt gat att 336
Ser Phe Asn Leu Tyr Asp Ala Thr Ser Ser Ser Thr Arg Ser Asp Ile
             100             105             110

ttt aaa aaa tat aaa gac aat aag act ata aat atg aaa gat ttc agc 384
Phe Lys Lys Tyr Lys Asp Asn Lys Thr Ile Asn Met Lys Asp Phe Ser
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414

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 35 40 45
 Lys Ile Asp Lys Pro Ile Phe Thr Ile Gln Glu Phe Asp Phe Lys Ile
 50 55 60
 Arg Gln Tyr Leu Met Gln Thr Tyr Lys Ile Tyr Asp Pro Asn Ser Pro
 65 70 75 80
 Tyr Ile Lys Gly Gln Leu Glu Ile Ala Ile Asn Gly Asn Lys His Glu
 85 90 95
 Ser Phe Asn Leu Tyr Asp Ala Thr Ser Ser Ser Thr Arg Ser Asp Ile
 100 105 110
 Phe Lys Lys Tyr Lys Asp Asn Lys Thr Ile Asn Met Lys Asp Phe Ser
 115 120 125
 His Phe Asp Ile Tyr Leu Trp Thr Lys
 130 135